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Genetic Correlations Among Protein Yield, Productive Life, and Type Traits from the United States and Diseases Other than Mastitis from Denmark and Sweden

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ABSTRACT

Sire genetic evaluations for protein yield, productive life, and selected type traits from the US were correlated with sire evaluations for disease from Denmark and Sweden and were then adjusted to approximate genetic correlations. Disease categories from Denmark included reproductive diseases, foot and leg diseases, metabolic and digestive diseases, and all diseases other than mastitis. Genetic evaluations for Denmark were from separate analyses for each disease category using a multiple-trait sire model with first, second, and third lactations handled as multiple traits. Evaluations from Sweden for all diseases other than mastitis were from a single-trait sire model using only first lactations. In addition, Danish and Swedish genetic evaluations were regressed on US type evaluations to test for quadratic relationships. Relationships were based on 104 bulls with US and Danish evaluations (88 with US type) and 84 bulls with US and Swedish evaluations (83 with US type). Genetic correlations between US protein yield and diseases were unfavorable, but correlations were favorable between productive life and disease. Genetic correlations among US type and diseases were around zero, except for correlations with US dairy form (range –0.34 to –0.73). Genetic correlations calculated from residual correlations (adjusted for predicted transmitting abilities for milk) between productive life and diseases were favorable (range 0.29 to 0.51). Genetic correlations calculated from residual correlations (adjusted for predicted transmitting abilities for milk) between dairy form and diseases ranged from –0.10 to –0.53. Selection for increased productive life may reduce disease occurrences, but selection for higher dairy form scores will increase disease occurrences.

(**Key words**: diseases, yield, type traits, longevity)

Abbreviation key: **PL** = productive life.

INTRODUCTION

It is widely accepted (7, 10) that a genetic antagonism exists between milk yield in dairy cattle and disease incidence. However, selection for improved yield, especially protein yield, is economically justified (7). Likewise, disease incidence and severity warrants selection pressure if accurate recording is possible at a reasonable cost. When direct recording of disease incidence is difficult, other measures may be useful for indirect selection to improve disease resistance or at least moderate the undesirable response of disease that occurs with intense selection for yield (6, 7, 8, 9, 10).

Some possible traits that could be useful for indirect selection of improved disease resistance include measures of longevity such as productive life (**PL**) and measures of physical characteristics such as body weight, body condition, or linear type traits that reflect body structure. Selection for increased PL could reduce diseases because diseases are primary causes of premature culling. Selection for increased body condition or less change in body condition during the lactation may reduce metabolic diseases in dairy cattle. Veerkamp (13) outlined the phenotypic associations among metabolic and reproductive problems and various measures of energy balance. Negative energy balance had a phenotypic association with several disorders. Some authors (4, 13) have suggested that physical traits including body weight could be used to select for improved feed efficiency. Selection to reduce body weight in an effort to improve feed efficiency is justified unless selection to reduce body weight results in substantial increases in

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disease occurrences. Selection for smaller body weight or size (along with selection to increase yield) may lead to more metabolic stress and may increase the frequency of metabolic and reproductive diseases. Any results of simultaneous selection for increased yield and smaller body size would depend on the genetic correlations among body size, yield, and diseases, which are largely unreported (13). Indeed, estimates of genetic relationships among PL, body dimensions, type traits, and diseases are needed to properly utilize these traits in breeding programs.

Currently in the US and some other countries, some selection occurs for increased body size and increased angularity or dairy character. This selection is due to the emphasis placed on selection for increased yield but also is due to selection based on type traits. Selection for higher type scores essentially places a small direct emphasis on increased body size and increased angularity. Perhaps more important, angularity or dairy character has been used to help identify dams of bulls destined for progeny test programs.

The objectives of this paper are to estimate genetic relationships among protein yield, PL, and type traits that reflect body and locomotive characteristics from the US and diseases other than mastitis from Denmark and Sweden. The objectives include characterization of quadratic relationships among genetic evaluations for diseases other than mastitis and linear type traits that reflect body and locomotive characteristics.

MATERIALS AND METHODS

Official sire evaluations from the US (July 1995) for production traits, PL, and type traits (from USDA-DHIA, Beltsville, MD and Holstein Association, Brattleboro, VT) were used in estimating the genetic correlations. Details of the US genetic evaluations can be found elsewhere (11, 12, 14). Traits were summarized using animal models with heritabilities ranging from 0.085 (for PL) to 0.42 (for stature). Heritability for protein yield was 0.25.

Official sire evaluations from Sweden for diseases other than mastitis (July 1995) were also used in the analyses. Genetic evaluations from Sweden include information from all diseases other than mastitis (composite trait) analyzed as a binomial trait. Veterinary treatments and fertility treatments by artificial insemination technicians from 10 d before first calving to 150 d after first calving were considered. The evaluations were calculated using a single-trait sire model with relationships (sire and maternal grandsire) and a heritability of 0.02 (3).

Unofficial sire evaluations from Denmark for diseases other than mastitis were also used in the analyses. Danish evaluations were calculated with data for Danish Black and White cattle from the Danish health recording system using a multiple-trait sire model that included lactations 1, 2, and 3 as separate traits. The model included the effects of herd and year of calving, year and month of calving, calving age, heterosis (to account for crossing North American Holsteins and Danish Friesians), sire (random), and residual. Relationships among sires through sire paths were included. Sire evaluations (from separate analyses) were available based on all diseases other than mastitis (composite trait, defined similarly to the Swedish trait), reproductive diseases, feet and leg diseases, and digestive and metabolic diseases. Heritabilities were all around 0.02, and genetic correlations between the lactations for each disease trait were large. Disease incidence was defined as 1, 2, or ≥ 3 episodes in a lactation. The lactation period was defined as 10 d before calving until d 305 of lactation. Danish evaluations from the analyses were multiplied by 10 and reversed in sign before use in computation of correlations and regressions. As a consequence, higher values for Danish genetic evaluations were favorable and reflected a lower disease frequency, which was also true for the Swedish evaluations. More details on the data, genetic parameters, and the method for calculating the genetic evaluations can be found in Sander-Nielsen et al. (9).

Sire genetic evaluations from the US were merged with sire genetic evaluations from Denmark to establish a file that included bulls with evaluations and daughters in both countries (i.e., US-Denmark file). An international cross-reference file established by the INTERBULL Centre (Uppsala, Sweden) was used to facilitate file merges. The same procedure was used to establish a file that included bulls with evaluations and daughters in Sweden and the US (i.e., US-Sweden file). Genetic correlations were estimated by adjusting product-moment correlations among sire evaluations for reliabilities (1). Each genetic correlation was calculated by dividing the product-moment correlation among sire evaluations for the two traits by the square root of the product of the mean reliabilities for the two traits involved. The correlation between daughter deviations on two traits, for which one trait is measured for one group of daughters and the second trait is measured for a second group of daughters sired by the same bulls, is an estimate of the genetic correlation. The method of Calo et al. (1) uses this concept but relies on genetic evaluations instead of daughter deviations. The method eliminates the impact of having genetic evaluations

regressed toward the mean (compared with daughter deviations) when the reliability of the genetic evaluations is less than 1.0. Residual correlations after adjusting for birth-year of the bull to eliminate the effect of genetic trend on correlation estimates were also calculated but not reported because they were very similar to the product-moment correlations. Genetic trend in the traits can bias genetic correlations estimated using genetic evaluations from independent daughter groups. Adjustment for birth year would likely eliminate the impact of genetic trend and any potential bias in the correlations that might result from genetic trend. Residual correlations among Danish and Swedish traits and US PL and dairy form after adjusting for PTA milk yield were also calculated, and genetic correlations calculated from these residual correlations are reported. In addition, genetic evaluations for disease data from Denmark and Sweden were regressed in separate models on US type traits to test for linear and quadratic relationships.

Genetic evaluations from the US and from Denmark or Sweden are from independent daughter groups, so only genetic covariance should be responsible for the correlations among progeny group performance. Edits were made to include only sires with 50 daughter equivalents for all disease traits in Denmark and reliability for PL from the US of 0.60 or greater or, in the case of matches with type, reliability for linear type of 0.70 or greater when creating the US-Denmark file. Edits were made to include only sires with 50 daughter equivalents in Sweden and reliability for PL from the US of 0.60 or greater or, in the case of matches with type, reliability for linear type of 0.70 or greater when creating the US-Sweden file. The same data were used for the regression analyses. Genetic correlations calculated from evaluations on sires with 125 daughter equivalents or more in Denmark or Sweden were made but not reported because these genetic correlations were very similar to those calculated from evaluations on sires with 50 daughter equivalents or more. Correlations with diseases in the third lactation from Denmark were also not reported because they were almost identical to the correlations involving diseases in second lactation. Genetic correlations between diseases in second and third lactations in Denmark are very high (9). One undesirable characteristic of the estimation procedure is the potential to get estimates outside the parameter space due to the adjustment for reliabilities, which can accentuate sampling effects. This problem diminishes as reliabilities of the evaluations increase. At the limit for reliabilities, the correlations among genetic evaluations from separate data sources represent the estimated genetic correlation. Stability of the estimates across various edits increases the confidence associated with the estimates. Utilizing genetic evaluations from independent daughter groups to calculate genetic correlations allows one to approximate partial genetic correlations (genetic correlations after the removal of the genetic contribution of another trait) and to calculate genetic regressions.

RESULTS AND DISCUSSION

Means, standard deviations, and descriptions for the sire evaluations used in the study are in Table 1. For the Danish and Swedish traits, higher sire evaluations are more desirable. Mean reliabilities for the US traits were all 0.95 or greater. Mean reliabilities for the Danish evaluations were from 0.49 to 0.56 and depended on the trait and data subset (matched with US yield data or type data). Mean reliability for the Swedish trait was 0.51. Adjustments to product-moment correlations to obtain genetic correlations are dependent on these reliabilities. Product-moment correlations among the genetic evaluations can be calculated by multiplying the estimated genetic correlations by a factor that depends on the reliabilities of the traits involved. Product-moment correlations can be calculated by multiplying the genetic correlations by a factor that ranges from 0.74 to 0.69 in the US-Denmark file and by approximately 0.70 in the US-Sweden file. Adjustments to product-moment correlations to obtain genetic correlations were primarily a reflection of the mean reliabilities of the Danish and Swedish evaluations because the mean reliabilities for all US evaluations were very high.

Genetic correlations and genetic relationships calculated primarily from information on daughters of selected bulls may or may not be representative of the true genetic correlation in the population. However, the genetic relationships calculated using information from daughters of selected bulls is representative of the genetic relationships within the contemporary breeding population. In addition, it should be noted that the genetic correlations used to calculate across-country evaluations and conversions come primarily from information on selected bulls and their close relatives (similar subset of bulls used in this study).

Genetic correlations among PL and protein yield from the US and the composite trait that includes all diseases other than mastitis from Denmark and Sweden are in Table 2. Genetic correlations between protein yield and the composite disease traits were from –0.19 to –0.62 and unfavorable. These correlations agree in direction with other studies (5, 7, 9,

TABLE 1. Mean, standard deviation, and description for sire genetic evaluations from the US, Denmark, and Sweden.[1]

Traits	$\bar{X}$	SD	Higher values for the trait correspond to
US			
Protein yield, kg	1.65	10.4	Higher yield
Productive life, mo	0.497	1.32	Longer life
Final score	0.397	0.834	Higher final score
Rear legs side view	–0.135	1.27	More leg set
Foot angle	0.302	1.38	Steeper angle
Rump angle	–0.244	1.19	Lower pin setting
Rump width	0.235	1.33	Wider rump
Dairy form	0.441	1.08	More angularity
Body depth	0.289	1.32	More depth
Strength	0.184	1.33	More strength
Stature	0.252	1.24	More height
Danish[2]			
All diseases other than mastitis			
First lactation	–0.600	0.394	Less disease
Second lactation	–0.594	0.370	Less disease
Reproductive diseases			
First lactation	–0.202	0.168	Less disease
Second lactation	–0.201	0.186	Less disease
Foot and leg diseases			
First lactation	–0.088	0.112	Less disease
Second lactation	–0.066	0.080	Less disease
Digestive and metabolic diseases			
First lactation	–0.255	0.195	Less disease
Second lactation	–0.271	0.200	Less disease
Swedish[3]			
All diseases other than mastitis in first lactation	94.8	4.68	Less disease

[1]Data for US evaluations of protein yield and productive life and Danish evaluations of diseases are from 104 sires. Data from US evaluations of type are from 88 sires. Data from Swedish evaluations of diseases are from 84 sires.

[2]Disease incidence for each trait definition and lactation were scored 1, 2, or 3 (3 and greater were combined). Danish evaluations were multiplied by –10 to scale the evaluations to be equivalent to published evaluations (higher values favorable) in Denmark and Sweden.

[3]Standardized to a mean of 100 and standard deviation of five for population.

10), however, the correlations between protein yield and the Danish measures were higher than in most reports. The correlations between protein yield and the composite disease traits in Denmark were larger in magnitude than between protein yield and the composite disease trait from Sweden. The differing results could be due to sampling or variation in recording and sire evaluation methods. Of the 104 and 84 bulls in the US-Denmark and US-Sweden files, only 39 were common to both the US-Denmark and US-Sweden files. Correlations in this study with milk and fat yield (not reported) were similar to the correlations with protein yield.

Genetic correlations between PL and composite disease traits in Table 2 were favorable and ranged from 0.16 to 0.39. The PL evaluations from the US had very high reliabilities (mean > 0.95), so essentially all of the information in the PL evaluations would have been direct information on daughter PL (PL evaluations on bulls in this study would have little influence from the correlated traits used in calculating US PL evaluations). Correlations between PL on bulls with early first-crop progeny and disease might not be the same as those reported here because PL evaluations on newly evaluated bulls are impacted by type traits used to predict PL. Many of these type traits may have little predictive value for diseases other than mastitis.

Genetic correlations between selected type traits from the US and the composite disease traits from Denmark and Sweden are in Table 2. Most correlations were near zero or were not consistently positive or negative. This result might be expected because the composite disease traits are a reflection of many different types of diseases. One exception was found; the correlations between dairy form and the composite disease traits were all substantial and negative

TABLE 2. Approximate genetic correlations among productive life, protein yield, and selected type traits from the US and all diseases other than mastitis from Denmark and Sweden.[1]

	All diseases other than mastitis		
US trait	First lactation in Denmark	Second lactation in Denmark	First lactation in Sweden
Protein yield	–0.62*	–0.60*	–0.19
Productive life	0.16	0.23	0.39*
Final score	–0.20	–0.06	0.06
Rear legs side view	–0.15	–0.04	–0.04
Foot angle	0.05	0.09	0.09
Rump angle	0.20	0.05	–0.14
Rump width	–0.18	–0.06	0.20
Dairy form	–0.73*	–0.60*	–0.46*
Body depth	–0.25	0.00	0.03
Strength	–0.14	0.06	0.13
Stature	–0.13	0.09	0.15

[1]Correlations between US protein yield and productive life and Danish traits are based on data from 104 bulls. Correlations between US type traits and Danish traits are based on data from 88 bulls. Correlations between US protein yield and productive life and the Swedish trait are based on data from 84 bulls. Correlations between US type traits and the Swedish trait are based on data from 83 bulls. Edits were made to include only bulls with an approximate minimum of 50 daughter equivalents in the genetic evaluations for diseases and reliabilities for US productive life of 0.60 or greater or reliabilities for US linear type of 0.70 or greater. Because of scaling, higher values are desirable for the Danish and Swedish traits.

*Correlations among sire evaluations were different from 0 ($P < 0.05$).

(range –0.46 to –0.73). Dairy form is correlated with yield, so this result agrees with the correlations between protein yield and disease. Higher dairy form scores were genetically associated with increased disease frequency.

Genetic correlations among US traits and reproductive diseases, foot and leg diseases, and digestive and metabolic diseases from Denmark are in Table 3. Protein yield had a substantial antagonistic genetic correlation with all the disease categories. Selection for increased protein yield will likely lead to increased reproductive diseases, increased foot and leg diseases, and increased digestive and metabolic diseases. The increased stress that comes with higher yield apparently increases the frequency of all the major diseases in dairy cattle.

Genetic correlations among PL and reproductive diseases, foot and leg diseases, and digestive and metabolic diseases were all small but favorable. Correlations with reproductive diseases tended to be smaller than correlations with foot and leg diseases or digestive and metabolic diseases. Selection for increased PL may lead to decreased disease frequency in dairy cattle. Productive life in the US is affected by yield (11) and has a positive correlation with yield traits (not adjusted for yield). The small positive correlations among PL and the disease traits exist in spite of the undesirable contribution from higher yield on diseases and the impact of yield on PL evaluations.

Genetic correlations among US PL and the disease traits calculated from residual correlations after adjustment for PTA milk yield are in Table 4. Correlations between disease traits and PL are all positive (range 0.29 to 0.51) and larger than the corresponding genetic correlations calculated from product-moment correlations among sire evaluations. The genetic component of PL that is independent of milk yield has a higher correlation with disease traits than

TABLE 3. Approximate genetic correlations among productive life, protein yield, and selected type traits from the US and reproductive diseases, foot and leg diseases, and digestive and metabolic diseases from Denmark.[1]

	Reproductive diseases		Foot and leg diseases		Digestive and metabolic diseases	
US trait	lactation 1	lactation 2	lactation 1	lactation 2	lactation 1	lactation 2
Protein yield	–0.52*	–0.62*	–0.47*	–0.46*	–0.43*	–0.30*
Productive life	0.08	0.12	0.19	0.18	0.17	0.24
Final score	–0.21	–0.16	–0.09	–0.02	–0.06	0.06
Rear legs side view	–0.14	–0.07	–0.07	–0.02	–0.11	–0.08
Foot angle	–0.02	–0.06	–0.01	–0.05	0.11	0.12
Rump angle	0.08	–0.08	0.39*	0.40*	0.16	0.09
Rump width	–0.08	–0.13	–0.20	–0.05	–0.13	0.02
Dairy form	–0.64*	–0.61*	–0.50*	–0.38*	–0.55*	–0.34*
Body depth	–0.19	–0.13	–0.28*	–0.12	–0.11	0.13
Strength	–0.09	–0.04	–0.20	–0.08	–0.05	0.12
Stature	–0.09	–0.04	–0.13	–0.02	–0.02	0.19

[1]Correlations between US protein yield and productive life and Danish traits are based on data from 104 bulls. Correlations between US type traits and Danish traits are based on data from 88 bulls. Edits were made to include only bulls with an approximate minimum of 50 daughter equivalents in the genetic evaluations for diseases and reliabilities for US productive life of 0.60 or greater or reliabilities for US linear type of 0.70 or greater. Because of scaling, higher values are desirable for the Danish traits.

*Correlations among sire evaluations were different from 0 ($P < 0.05$).

TABLE 4. Approximate genetic correlations among productive life and dairy form from the US and diseases other than mastitis from Denmark and Sweden calculated from residual correlations among sire genetic evaluations after adjustment for PTA milk yield.[1]

	US	
	Productive life	Dairy form
All diseases other than mastitis		
First lactation in Sweden	0.51*	–0.42*
First lactation in Denmark	0.43*	–0.53*
Second lactation in Denmark	0.51*	–0.33*
Reproductive diseases		
First lactation in Denmark	0.29*	–0.50*
Second lactation in Denmark	0.37*	–0.42*
Foot and leg diseases		
First lactation in Denmark	0.36*	–0.34*
Second lactation in Denmark	0.35*	–0.17
Digestive and metabolic diseases		
First lactation in Denmark	0.36*	–0.33*
Second lactation in Denmark	0.41*	–0.10

[1]Correlations between US productive life and Danish traits are based on data from 104 bulls. The correlation between US productive life and the Swedish trait is based on data from 84 bulls. Correlations between US dairy form and Danish traits are based on data from 88 bulls. The correlation between US dairy form and the Swedish trait is based on data from 88 bulls. Edits were made to include only bulls with an approximate minimum of 50 daughter equivalents in the genetic evaluations for diseases and reliabilities for US productive life of 0.60 or greater or reliabilities for US linear type of 0.70 or greater. Because of scaling, higher values are desirable for the Danish and Swedish traits.

*Correlations among sire evaluations were different from 0 ($P < 0.05$).

the unadjusted PL. Inclusion of PL in the US breeding program in the absence of direct evaluations for diseases will likely have a desirable impact on diseases other than mastitis.

Most genetic correlations among selected type traits and reproductive diseases, foot and leg diseases, and digestive and metabolic diseases were small and did not indicate important relationships between type and the diseases in this study. However, as with the case for the composite disease traits, the correlations between dairy form and the three disease categories (reproductive diseases, foot and leg diseases, and digestive and metabolic diseases) were all negative (range –0.34 to –0.64). It is interesting to note that correlations of rump width, body depth, strength, and stature with reproductive diseases, foot and leg diseases, and digestive and metabolic diseases also tend to be negative or near zero. Selection for high dairy form scores may substantially increase diseases other than mastitis in dairy cattle. In addition, selection for wider rumps, deeper bodies, more strength, and taller cows will likely have little positive impact on disease resistance. In this study, there was no indication that genetically larger body size or more strength would be advantageous from a disease perspective. These results indicate that selection for smaller body size and increased yield to improve feed efficiency will not likely increase disease incidence. One might speculate that selection for smaller body size might result in more metabolic stress and increased metabolic diseases, but these results do not support such speculation.

Genetic correlations between disease traits and dairy form calculated from residual correlations after adjustment for PTA milk yield (Table 4) are all negative and tend to be moderate in magnitude (range –0.10 to –0.53). These results indicate that dairy form has a significant association with diseases other than mastitis, especially reproductive diseases, that is independent of milk yield. The results of this study are especially troublesome because dairy form or a closely related trait is often utilized to choose cows as bull dams. Often, cows with higher dairy form scores are selected as bull dams when most other available criteria are similar. Dairy form scores are essentially utilized to confirm the accuracy of recorded production. In addition, selection for higher type scores essentially places a small direct emphasis on increased angularity. Based on these results, selection for higher dairy form may be indirectly selecting for cows that are more prone to reproductive diseases, foot and leg diseases, and digestive and metabolic diseases. Higher dairy form scores may be a reflection of subclinical metabolic disease and selection for higher dairy form scores may increase associated disease frequency. Perhaps dairy form could be used as a marker for improved disease resistance, but the direction of selection would be opposite of what is currently practiced. Selection for lower dairy form scores would only be reasonable if intense selection for recorded milk yield was practiced because dairy form and milk yield are correlated. The current direct selection for milk yield and simultaneous indirect selection for yield based on dairy form is likely counter to improving disease resistance in dairy populations. Measured milk, protein, and fat yields probably should be the only traits used for improving yields; correlated body traits should be used with caution.

The quadratic regression of reproductive diseases in second lactation from Denmark on dairy form was the only significant ($P < 0.05$) quadratic regression found in these analyses (Figure 1). Although not significant ($P = 0.15$), the quadratic regression of reproductive diseases in first lactation from Denmark on dairy form was similar in shape. Linear regression

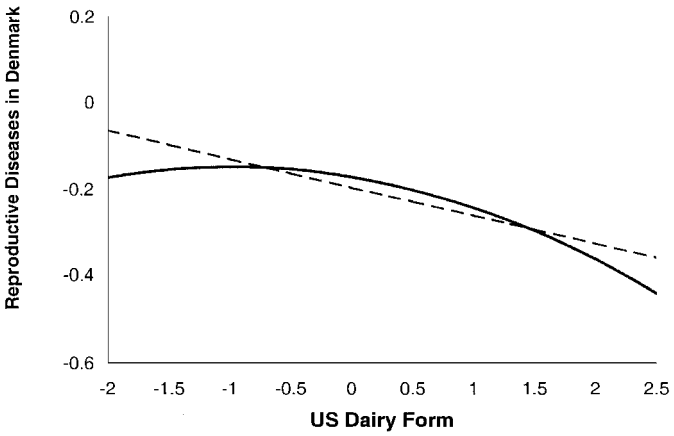

Figure 1. Regression of Danish sire evaluations for reproductive diseases in second lactation on US sire evaluations for dairy form. Lines represent linear (. . .) and quadratic regressions (–) and are based on data from 88 bulls with Danish and US genetic evaluations. Edits were made to include only bulls with an approximate minimum of 50 daughter equivalents in Danish disease evaluations and reliabilities for US type of 0.70 or greater. Danish sire evaluations had a mean of –0.22 and the standard deviation of 0.17 for these 88 bulls (range from –0.80 to 0.16). The US genetic evaluations for dairy form had a mean of 0.44, and the standard deviation was 1.08 for these 88 bulls (range from –2.23 to 3.04).

of reproductive diseases in second lactation in Denmark on dairy form had an intercept of –0.20 and a linear coefficient of –0.066 (SE = 0.015). The quadratic regression of reproductive diseases in second lactation in Denmark on dairy form had an intercept of –0.17, a linear coefficient of –0.048 (SE = 0.017), and a quadratic coefficient of –0.024 (SE = 0.011). The quadratic relationship between reproductive diseases in Denmark and dairy form indicated that as dairy form scores increased, reproductive diseases tended to increase at an increasing rate. Those bulls with very high dairy form scores had daughters with the most reproductive disease problems.

Correlations among foot angle and reproductive diseases, foot and leg diseases, and digestive and metabolic diseases tended to be very low, which does not support other reports (8). Other studies (7, 8) have found important relationships among foot traits and various measures of health. Correlations between rump angle and foot and leg diseases were moderate and positive. More slope from hooks to pins was favorably associated with foot and leg diseases. Dutch workers (2) found that more slope was also associated with decreased calving difficulty. Perhaps selection for more slope to the rump can be justified for maternal calving ease and for improved foot and leg health.

With the exception of the quadratic regression of reproductive diseases from Denmark on dairy form, quadratic genetic relationships among the diseases and the selected type traits were not important. Although intermediate optimums may exist at the phenotypic level for some type traits in relation to disease incidence, we found little evidence in this study to indicate that breeding programs should select or mate to produce animals with intermediate genetic values for the type traits that reflect locomotion or body characteristics.

CONCLUSIONS

A substantial antagonistic genetic relationship exists between protein yield and diseases other than mastitis. A desirable genetic correlation exists between US PL and diseases other than mastitis (especially if the effect of milk yield on PL and disease is removed). Selection for increased PL may have a desirable impact on the frequency of diseases other than mastitis in US Holsteins.

Results from this study indicate that the genetic correlations between most type traits and diseases other than mastitis are small. Traits that are exceptions to this general result include dairy form and rump angle. In this study, more slope from hooks to pins was genetically associated with less frequent foot and leg diseases. Likely more important, the genetic correlations between dairy form and diseases were unfavorable. Selection for higher dairy form scores may substantially increase diseases other than mastitis and may compound the undesirable response in diseases other than mastitis that accompanies selection for increased yield. Current practices of using dairy form or equivalent information for final decisions in bull dam selection or in sire selection should be reevaluated.

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